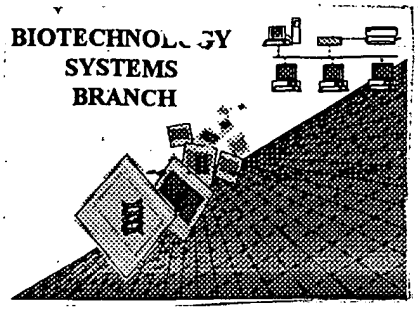
Nickol

BIOTECHNOLOGY SYSTEMS BRANCH



RECEIVED

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TECH CENTER 1600/2900

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/451,739B

Source: 1642

Date Processed by STIC: 1/2/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

http://www.uspto.gov/web/offices/pac/checker

Application No.: 09/451739

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- [X] 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- [ ] 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- [ ] 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- [ ] 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- [X] 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- [ ] 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- [ ] 7. Other: _____

Applicant Must Provide:

- [X] An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- [X] An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- [X] A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
PatentIn Software Program Support
Technical Assistance.....703-287-0200
To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION SERIAL NUMBER: 09/457,239B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 ____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 ____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 ____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 ____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 ____ Variable Length
Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7 ____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

8 ____ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 ____ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 ____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 ____ Use of <220>Feature (NEW RULES)
Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13 ____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

G. Nickol

1642

RAW SEQUENCE LISTING DATE: 01/02/2001
PATENT APPLICATION: US/09/451,739B TIME: 11:02:39

Input Set : A:\ES.txt
Output Set: N:\CRF3\01022001\I451739B.raw

see item 5 on Error Summary Sheet.

1 <110> APPLICANT: Jager, Dirk
2 Scanlan, Matthew
3 Gure, Ali
4 Jager, Elke
5 Knuth, Alexander
6 Old, Lloyd
7 Chen, Yao-tseng
9 <120> TITLE OF INVENTION: Isolated Nucleic Acid Molecules Encoding Cancer Associated
10 Antigens,
11 the Antigens per se, and Uses Thereof
13 <130> FILE REFERENCE: LUD 5615
15 <140> CURRENT APPLICATION NUMBER: 09/451,739B
17 <141> CURRENT FILING DATE: 1999-11-30
19 <160> NUMBER OF SEQ ID NOS: 19

ERRORED SEQUENCES

520 <210> SEQ ID NO: 16
521 <211> LENGTH: 513 512 shown (next page)
522 <212> TYPE: PRT
523 <213> ORGANISM: Homo sapiens
OK -> 524 <400> SEQUENCE: 16
525 Met Lys Val Ser Ile Pro Thr Lys Ala Leu Glu Leu Met Asp Met Gln
526 1 5 10 15
528 Thr Phe Lys Ala Glu Pro Pro Glu Lys Pro Ser Ala Phe Glu Pro Ala
529 20 25 30
531 Ile Glu Met Gln Lys Ser Val Pro Asn Lys Ala Leu Glu Leu Lys Asn
532 35 40 45
534 Glu Gln Thr Leu Arg Ala Asp Glu Ile Leu Pro Ser Glu Ser Lys Gln
535 50 55 60
537 Lys Asp Tyr Glu Glu Ser Ser Trp Asp Ser Glu Ser Leu Cys Glu Thr
538 65 70 75 80
540 Val Ser Gln Lys Asp Val Cys Leu Pro Lys Ala Thr His Gln Lys Glu
541 85 90 95
543 Ile Asp Lys Ile Asn Gly Lys Leu Glu Glu Ser Pro Asp Asn Asp Gly
544 100 105 110
547 Phe Leu Lys Ala Pro Cys Arg Met Lys Val Ser Ile Pro Thr Lys Ala
548 115 120 125
550 Leu Glu Leu Met Asp Met Gln Thr Phe Lys Ala Glu Pro Pro Glu Lys
551 130 135 140
553 Pro Ser Ala Phe Glu Pro Ala Ile Glu Met Gln Lys Ser Val Pro Asn
554 145 150 155 160
556 Lys Ala Leu Glu Leu Lys Asn Glu Gln Thr Leu Arg Ala Asp Gln Met
557 165 170 175
559 Phe Pro Ser Glu Ser Lys Gln Lys Lys Val Glu Glu Asn Ser Trp Asp
560 180 185 190

RAW SEQUENCE LISTING DATE: 01/02/2001
PATENT APPLICATION: US/09/451,739B TIME: 11:02:39

Input Set : A:\ES.txt
Output Set: N:\CRF3\01022001\I451739B.raw

```
     562 Ser Glu Ser Leu Arg Glu Thr Val Ser Glu Lys Asp Val Cys Val Pro
     563         195                 200                 205
     565 Lys Ala Thr His Gln Lys Glu Met Asp Lys Ile Ser Gly Lys Leu Glu
     566     210                 215                 220
     568 Asp Ser Thr Ser Leu Ser Lys Ile Leu Asp Thr Val His Ser Cys Glu
     569 225                 230                 235                 240
     571 Arg Ala Arg Glu Leu Gln Lys Asp His Cys Glu Gln Arg Thr Gly Lys
E--> 572             ~~245~~ 245         ~~250~~ 250         ~~255~~ 255
     574 Met Glu Gln Met Lys Lys Lys Phe Cys Val Leu Lys Lys Lys Leu Ser
E--> 575         ~~260~~ 260         ~~265~~ 265         ~~270~~ 270
     577 Glu Ala Lys Glu Ile Lys Ser Gln Leu Glu Asn Gln Lys Val Lys Trp
E--> 578     275                 280                 285
     580 Glu Gln Glu Leu Cys Ser Val Arg Leu Thr Leu Asn Gln Glu Glu Glu
E--> 581 290                 295                 300                 305
     583 Lys Arg Arg Asn Ala Asp Ile Leu Asn Glu Lys Ile Arg Glu Glu Leu
E--> 584                 310                 315                 320
     586 Gly Arg Ile Glu Glu Gln His Arg Lys Glu Leu Glu Val Lys Gln Gln
E--> 587             325                 330                 335
     589 Leu Glu Gln Ala Leu Arg Ile Gln Asp Ile Glu Leu Lys Ser Val Glu
E--> 590         340                 345                 350
     592 Ser Asn Leu Asn Gln Val Ser His Thr His Glu Asn Glu Asn Tyr Leu
E--> 593     355                 360                 365
     595 Leu His Glu Asn Cys Met Leu Lys Lys Glu Ile Ala Met Leu Lys Leu
E--> 596 370                 375                 380                 385
     598 Glu Ile Ala Thr Leu Lys His Gln Tyr Gln Glu Lys Glu Asn Lys Tyr
E--> 599                 390                 395                 400
     601 Phe Glu Asp Ile Lys Ile Leu Lys Glu Lys Asn Ala Glu Leu Gln Met
E--> 602             405                 410                 415
     604 Thr Leu Lys Leu Lys Glu Glu Ser Leu Thr Lys Arg Ala Ser Gln Tyr
E--> 605         420                 425                 430
     607 Ser Gly Gln Leu Lys Val Leu Ile Ala Glu Asn Thr Met Leu Thr Ser
E--> 608     435                 440                 445
     610 Lys Leu Lys Glu Lys Gln Asp Lys Glu Ile Leu Glu Ala Glu Ile Glu
E--> 611 450                 455                 460                 465
     613 Ser His His Pro Arg Leu Ala Ser Ala Val Gln Asp His Asp Gln Ile
E--> 615                 470                 475                 480
     617 Val Thr Ser Arg Lys Ser Gln Glu Pro Ala Phe His Ile Ala Gly Asp
E--> 618             485                 490                 495
     620 Ala Cys Leu Gln Arg Lys Met Asn Val Asp Val Ser Ser Thr Asp Ile
E--> 621         500                 505                 510
```

misalgied amino acid numbers (see item 4 on Error Summary Sheet)

see next page for more errors

<210> 1
<211> 1533
<212> DNA
<213> Homo sapiens
<220>
<221> CDS
<222> 235
<400> 1

ggttttccac gttggacaag tgcggctcgg cggccagcgg agcgcgcccc ttcccgctgc 60

ccgctccgct cctctcttct acccagccca gtgggcgagt gggcagcggc ggccgcggcg 120

ctgggccctc tcccgccggt gtgtgcgcgc tcgtacgcgc ggcccccggc gccagccccg 180

ccgcctgaga gggggcctgc gccgccggcc ggggcgtgcg cccgggagcc accgncaccg 240

cggcccgcgc cctcaggcgc tggggtcccc gcggacccgg aggcggcgga cgggctcggc 300

agatgtagcc gccgggccga agcaggagcc ggcgggggggg cgccgggaga gcgagggctt 360

tgcattttgc agtgctattt tttgaggggg gcggagggtg gaggaagtcg gaaagccgcg 420

ccgagtcgcc ggggacctcc ggggtgaacc atgttgagtc ctgccaacgg ggagcagctc 480

cacctggtga actatgtgga ggactacctg gactccatcg agtccctgcc tttcgacttg 540

cagagaaatg tctcgctgat gcgggagatc gacgcgaaat accaagagat cctgaaggag 600

ctagacgagt gctacgagcg cttcagtcgc gagacagacg gggcgcagaa gcggcggatg 660

ctgcactgtg tgcagcgcgc gctgatccgc agccaggagc tgggcgacga gaagatccag 720

atcgtgagcc agatggtgga gctggtggag aaccgcacgc ggcaggtgga cagccacgtg 780

gagctgttcg aggcgcagca ggagctgggc gacacagcgg gcaacagcgg caaggctggc 840

gcggacaggc ccaaaggcga ggcggcagcg caggctgaca agcccaacag caagcgctca 900

cggcggcagc gcaacaacga gaaccgtgag aacgcgtcca gcaaccacga ccacgacgac 960

ggcgcctcgg gcacacccaa ggagaagaag gccaagacct ccaagaagaa gaagcgctcc 1020

aaggccaagg cggagcgaga ggcgtcccct gccgacctcc ccatcgaccc caacgaaccc 1080

acgtactgtc tgtgcaacca ggtctcctat ggggagatga tcggctgcga caacgacgag 1140

tgccccatcg agtggttcca cttctcgtgc gtggggctca atcataaacc caagggcaag 1200
tggtactgtc ccaagtgccg gggggagaac gagaagacca tggacaaagc cctggagaaa 1260

tccaaaaaag agagggctta caacaggtag tttgtggaca ggcgcctggt gtgaggagga 1320

caaaataaac cgtgtattta ttacattgct gcctttgttg aggtgcaagg agtgtaaaat 1380

gtatattttt aaagaatgtt agaaaaggaa ccattccttt catagggatg gcagtgattc 1440

tgtttgcctt ttgttttcat tggtacacgt gtaacaagaa agtggtctgt ggatcagcat 1500

tttagaaact acaaatatag gtttgattca aca 1533

7 see item 10 on Error Summary Sheet

FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 01/02/2001
PATENT APPLICATION: US/09/451,739B TIME: 11:02:40

Input Set : A:\ES.txt
Output Set: N:\CRF3\01022001\I451739B.raw

L:26 M:283 W: Missing Blank Line separator, <220> field identifier
L:29 M:283 W: Missing Blank Line separator, <400> field identifier
L:36 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:36 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:87 M:283 W: Missing Blank Line separator, <400> field identifier
L:133 M:283 W: Missing Blank Line separator, <220> field identifier
L:134 M:283 W: Missing Blank Line separator, <400> field identifier
L:167 M:283 W: Missing Blank Line separator, <400> field identifier
L:203 M:283 W: Missing Blank Line separator, <400> field identifier
L:264 M:283 W: Missing Blank Line separator, <220> field identifier
L:265 M:283 W: Missing Blank Line separator, <400> field identifier
L:314 M:283 W: Missing Blank Line separator, <400> field identifier
L:367 M:283 W: Missing Blank Line separator, <400> field identifier
L:390 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:390 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:390 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
L:399 M:283 W: Missing Blank Line separator, <400> field identifier
L:407 M:283 W: Missing Blank Line separator, <400> field identifier
L:415 M:283 W: Missing Blank Line separator, <400> field identifier
L:423 M:283 W: Missing Blank Line separator, <400> field identifier
L:431 M:283 W: Missing Blank Line separator, <400> field identifier
L:439 M:283 W: Missing Blank Line separator, <400> field identifier
L:450 M:283 W: Missing Blank Line separator, <400> field identifier
L:505 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:505 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:505 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
L:509 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:509 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
M:340 Repeated in SeqNo=15
L:513 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:513 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:515 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:515 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:517 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:15
L:517 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:524 M:283 W: Missing Blank Line separator, <400> field identifier
L:572 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
M:332 Repeated in SeqNo=16
L:621 M:252 E: No. of Seq. differs, <211>LENGTH:Input:513 Found:512 SEQ:16
L:628 M:283 W: Missing Blank Line separator, <400> field identifier
L:636 M:283 W: Missing Blank Line separator, <400> field identifier
L:644 M:283 W: Missing Blank Line separator, <400> field identifier